

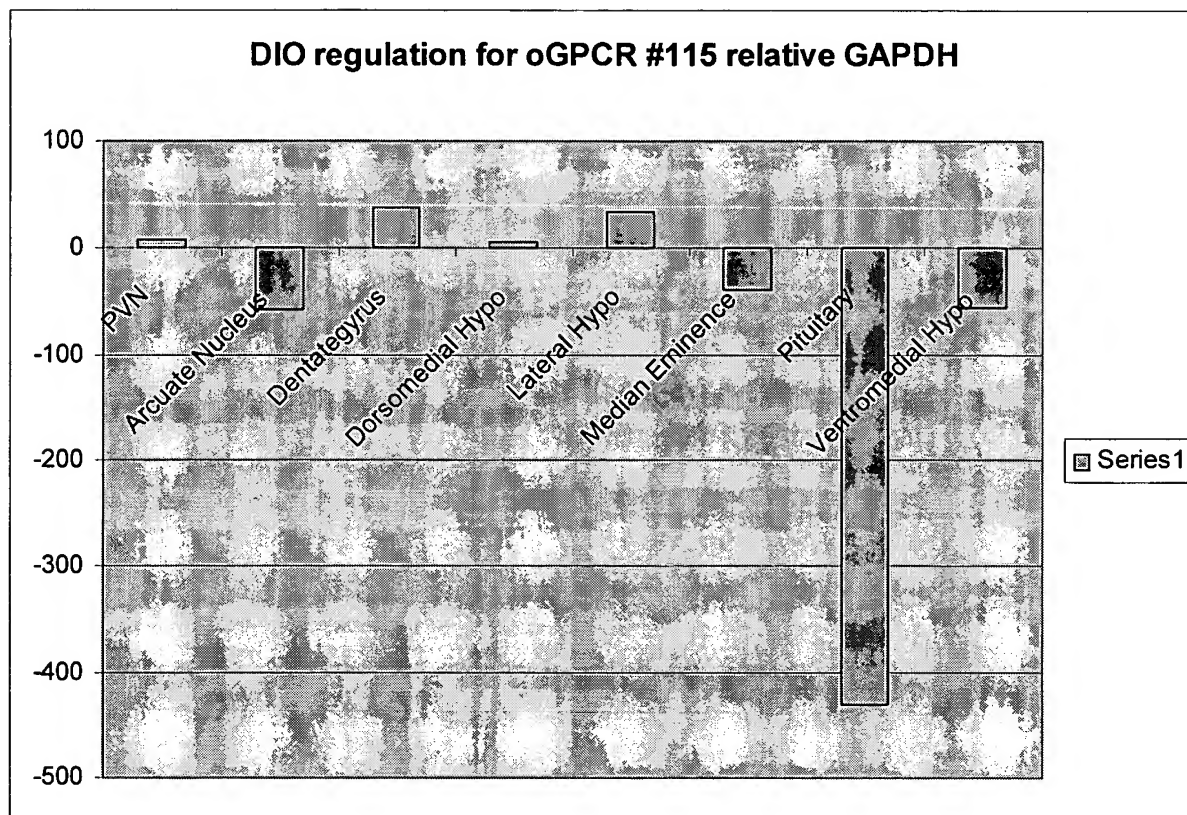
FIG. 1 : SEQ ID NO:1 -

ATG AAC TCG TGG GAC GCG GGC CTG GCG GGG CTA CTG GTG GGC ACG ATG	48
GGC GTC TCG CTG CTG TCC AAC GCG CTG GTG CTG CTC TGC CTG CTG CAC	96
AGC GCG GAC ATC CGC CGC CAG GCG CCG GCG CTC TTC ACC CTG AAC CTC	144
ACG TGC GGG AAC CTG CTG TGC ACC GTG GTC AAC ATG CCG CTC ACG CTG	192
GCC GGC GTC GTG GCG CAG CGG CAG CCG GCG GGC GAC CGC CTG TGC CGC	240
CTG GCT GCC TTC CTC GAC ACC TTC CTG GCT GCC AAC TCC ATG CTC AGC	288
ATG GCC GCG CTC AGC ATC GAC CGC TGG GTG GCC GTG GTC TTC CCG CTG	336
AGC TAC CGG GCC AAG ATG CGC CTC CGC GAC GCG GCG CTC ATG GTG GCC	384
TAC ACG TGG CTG CAC GCG CTC ACC TTC CCA GCC GCC GCG CTC GCC CTG	432
TCC TGG CTC GGC TTC CAC CAG CTG TAC GCC TCG TGC ACG CTG TGC AGC	480
CGG CGG CCA GAC GAG CGC CTG CGC TTC GCC GTC TTC ACT GGC GCC TTC	528
CAC GCT CTC AGC TTC CTG CTC TCC TTC GTC GTG CTC TGC TGC ACG TAC	576
CTC AAG GTG CTC AAG GTG GCC CGC TTC CAT TGC AAG CGC ATC GAC GTG	624
ATC ACC ATG CAG ACG CTG GTG CTG CTG GTG GAC CTG CAC CCC AGT GTG	672
CGG GAA CGC TGT CTG GAG GAG CAG AAG CGG AGG CGA CAG CGA GCC ACC	720
AAG AAG ATC AGC ACC TTC ATA GGG ACC TTC CTT GTG TGC TTC GCG CCC	768
TAT GTG ATC ACC AGG CTA GTG GAG CTC TTC TCC ACG GTG CCC ATC GGC	816
TCC CAC TGG GGG GTG CTG TCC AAG TGC TTG GCG TAC AGC AAG GCC GCA	864
TCC GAC CCC TTT GTG TAC TCC TTA CTG CGA CAC CAG TAC CGC AAA AGC	912
TGC AAG GAG ATT CTG AAC AGG CTC CTG CAC AGA CGC TCC ATC CAC TCC	960
TCT GGC CTC ACA GGC GAC TCT CAC AGC CAG AAC ATT CTG CCG GTG TCT	1008
GAG	1011

FIG. 2 : SEQ ID NO:2

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Met	16
Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His	32
Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu	48
Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu	64
Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg	80
Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser	96
Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu	112
Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala	128
Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu	144
Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser	160
Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe	176
His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr	192
Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val	208
Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val	224
Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr	240
Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro	256
Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly	272
Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala	288
Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser	304
Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser	320
Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser	336
Glu	337

FIG. 3



```

MOUSEGN_CHR7-36867   ATGAACTCGTGGGACGCGGGCCTGGCGGGGCTGCTGGTGGGCACTATCGGCGTGTGCGTG
SEQUENCE_115_        ATGAACTCGTGGGACGCGGGCCTGGCGGGGCTACTGGTGGGCACGATGGGCGTCTCGCTG
*****

MOUSEGN_CHR7-36867   CTGTCCAACGGGCTGGTGTGCTCTGCCTCCTGCACAGCGGTGACATCCGCCGCCAGGCG
SEQUENCE_115_        CTGTCCAACGGGCTGGTGTGCTCTGCCTGCTGCACAGCGCGGACATCCGCCGCCAGGCG
*****

MOUSEGN_CHR7-36867   CCGGCGCTCTTCACTCTCAACCTCACGTGTGGCAACCTGCTGTGTACCGTGGTCAACATG
SEQUENCE_115_        CCGGCGCTCTTCAACCTGAACCTCACGTGCGGGAACCTGCTGTGCACCGTGGTCAACATG
*****

MOUSEGN_CHR7-36867   CCACTAACTGGCCGGCGTCTGTGGCACAACGGCAGCCGGCCGGGGACCGCTGTGCCCG
SEQUENCE_115_        CCGCTCACGCTGGCCGGCGTCTGTGGCGCAGCGGCAGCCGGCGGGCGACCGCCTGTGCCCG
***

MOUSEGN_CHR7-36867   CTGGCCGCCTTCTCTGACACCTTTCTGGCCGCCAACTCCATGCTCAGCATGGCCGCGCTC
SEQUENCE_115_        CTGGCTGCCTTCTCTGACACCTTCTGGCTGCCAACTCCATGCTCAGCATGGCCGCGCTC
*****

MOUSEGN_CHR7-36867   AGCATCGACCGCTGGGTGGCTGTGGTCTTTCCGCTGAGCTACCGTGCCAAGATGCGCCTC
SEQUENCE_115_        AGCATCGACCGCTGGGTGGCGTGGTCTTCCGCTGAGCTACCGGGCCAAGATGCGCCTC
*****

MOUSEGN_CHR7-36867   CGAGATGCCGCCTTCATGGTGGCCTACACGTGGCTGCACGCGCTCACCTTCCGGCCACC
SEQUENCE_115_        CGGACGCGGCGCTCATGGTGGCCTACACGTGGCTGCACGCGCTCACCTTCCAGCCGCC
***

MOUSEGN_CHR7-36867   GCGCTCGCCCTGTCTGGCTCGGCTTCCACCAGCTATATGCCTCGTGACACTGTGCAGC
SEQUENCE_115_        GCGCTCGCCCTGTCTGGCTCGGCTTCCACCAGCTGTACGCTCGTGACGCTGTGCAGC
*****

MOUSEGN_CHR7-36867   CGGCGGCCGAGCAGCGCCTGCGCTTTGCTGTCTTACCAGCGCCTTCCATGCGCTCAGC
SEQUENCE_115_        CGGCGGCCAGACGAGCGCCTGCGCTTCGCCGTCTTACTGGCGCCTTCCACGCTCTCAGC
*****

MOUSEGN_CHR7-36867   TTCCTGCTCTCCTTCATCGTGCTCTGCTTACGTACCTCAAGGTGCTCAAGGTGGCCCGC
SEQUENCE_115_        TTCCTGCTCTCCTTCGTCGTCTGCTGTCACGTACCTCAAGGTGCTCAAGGTGGCCCGC
*****

MOUSEGN_CHR7-36867   TTCACTGCAAGCGCATCGACGTGATCACCATGCAGACGCTTGTGCTGTTGGTGGACATA
SEQUENCE_115_        TTCAATTGCAAGCGCATCGACGTGATCACCATGCAGACGCTGGTGTGCTGTTGGTGGACCTG
*****

MOUSEGN_CHR7-36867   CACCCAGTGTGAGGGAACGGTGTCTGGAGGAACAGAAGCGGAGGCGACAGCGTGCCACC
SEQUENCE_115_        CACCCAGTGTGCGGGAACGCTGTCTGGAGGAGCAGAAGCGGAGGCGACAGCGAGCCACC
*****

MOUSEGN_CHR7-36867   AAGAAGATCAGCACCTTCATAGGGACCTTCTTGTGTGCTTTCACCCCTATGTGATTACC
SEQUENCE_115_        AAGAAGATCAGCACCTTCATAGGGACCTTCTTGTGTGCTTTCGCGCCCTATGTGATCACC
*****

MOUSEGN_CHR7-36867   AGGCTGGTGGAACTCTTCTCCACAGCACCCATTGGCTCTCACTGGGGAGTGCTGTCCAAG
SEQUENCE_115_        AGGCTAGTGGAGCTCTTCTCCACGGTGCCCATCGGCTCCCACTGGGGGGTGCTGTCCAAG
*****

MOUSEGN_CHR7-36867   TGCTTGGCCTACAGCAAGGCCGCTTCTGACCCCTTCGTGTATTCTTGTGCTGCGACACCAA
SEQUENCE_115_        TGCTTGGCGTACAGCAAGGCCGCTATCCGACCCCTTGTGTACTCTTACTGCGACACCAA
*****

MOUSEGN_CHR7-36867   TACCGCAGGAGCTGCAAGGAGCTCCTGAACAGGATCTTCAACAGACGCTCCCTTCACTCT
SEQUENCE_115_        TACCGCAAAAGCTGCAAGGAGATTCTGAACAGGCTCCTGCACAGACGCTCCATCCACTCC
*****

MOUSEGN_CHR7-36867   GTGGGCCTCACAGGTGACTCTCACAGCCAGAACATTCTGCCAGTGTGGAA---
SEQUENCE_115_        TCTGGCCTCACAGGCGACTCTCACAGCCAGAACATTCTGCCGGTGTCTGAGTGA
*****

```

Figure 4: Alignment of human and mouse GPCR #115